

Manchipouri



RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/10/000,039A

TIME: 15:40:13

Input Set : N:\Crif3\RULE60\10000039A.RAW.txt

Output Set: N:\CRF4\07032003\J0000039A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: LANG, Florian

6 WALDEGGER, Tübingen

8 (ii) TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK

10 (iii) NUMBER OF SEQUENCES: 4

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: FOLEY & LARDNER

14 (B) STREET: 3000 K Street, N.W.

15 (C) CITY: Washington

16 (D) STATE: D.C.

17 (E) COUNTRY: U.S.A.

18 (F) ZIP: 20007-5109

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/000,039A

C--> 28 (B) FILING DATE: 04-Dec-2001

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

W--> 32 (A) APPLICATION NUMBER: US/09/031,295

33 (B) FILING DATE: 26-FEB-1998

W--> 35 (A) APPLICATION NUMBER: DE 197-08-173.8

36 (B) FILING DATE: 28-FEB-1997

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Sandercock, Colin G.

40 (B) REGISTRATION NUMBER: 31,298

41 (C) REFERENCE/DOCKET NUMBER: 058315/0123

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (202) 672-5300

45 (B) TELEFAX: (202) 672-5399

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2370 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

60 (A) NAME/KEY: CDS

ENTERED

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61          (B) LOCATION: 43..1335
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66 CACGAGGGAG CGCTAACGTC TTTCTGTCTC CCCGCGGTGG TG ATG ACG GTG AAA      54
67                                     Met Thr Val Lys
68                                     1
70 ACT GAG GCT GCT AAG GGC ACC CTC ACT TAC TCC AGG ATG AGG GGC ATG      102
71 Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg Met Arg Gly Met
72 5          10          15          20
74 GTG GCA ATT CTC ATC GCT TTC ATG AAG CAG AGG AGG ATG GGT CTG AAC      150
75 Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg Met Gly Leu Asn
76          25          30          35
78 GAC TTT ATT CAG AAG ATT GCC AAT AAC TCC TAT GCA TGC AAA CAC CCT      198
79 Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala Cys Lys His Pro
80          40          45          50
82 GAA GTT CAG TCC ATC TTG AAG ATC TCC CAA CCT CAG GAG CCT GAG CTT      246
83 Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln Glu Pro Glu Leu
84          55          60          65
86 ATG AAT GCC AAC CCT TCT CCT CCA CCA AGT CCT TCT CAG CAA ATC AAC      294
87 Met Asn Ala Asn Pro Ser Pro Pro Pro Ser Pro Ser Gln Gln Ile Asn
88          70          75          80
90 CTT GGC CCG TCG TCC AAT CCT CAT GCT AAA CCA TCT GAC TTT CAC TTC      342
91 Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe
92 85          90          95          100
94 TTG AAA GTG ATC GGA AAG GGC AGT TTT GGA AAG GTT CTT CTA GCA AGA      390
95 Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala Arg
96          105          110          115
98 CAC AAG GCA GAA GAA GTG TTC TAT GCA GTC AAA GTT TTA CAG AAG AAA      438
99 His Lys Ala Glu Glu Val Phe Tyr Ala Val Lys Val Leu Gln Lys Lys
100          120          125          130
102 GCA ATC CTG AAA AAG AAA GAG GAG AAG CAT ATT ATG TCG GAG CGG AAT      486
103 Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met Ser Glu Arg Asn
104          135          140          145
106 GTT CTG TTG AAG AAT GTG AAG CAC CCT TTC CTG GTG GGC CTT CAC TTC      534
107 Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His Phe
108          150          155          160
110 TCT TTC CAG ACT GCT GAC AAA TTG TAC TTT GTC CTA GAC TAC ATT AAT      582
111 Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu Asp Tyr Ile Asn
112 165          170          175          180
114 GGT GGA GAG TTG TTC TAC CAT CTC CAG AGG GAA CGC TGC TTC CTG GAA      630
115 Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg Cys Phe Leu Glu
116          185          190          195
118 CCA CGG GCT CGT TTC TAT GCT GCT GAA ATA GCC AGT GCC TTG GGC TAC      678
119 Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly Tyr
120          200          205          210
122 CTG CAT TCA CTG AAC ATC GTT TAT AGA GAC TTA AAA CCA GAG AAT ATT      726
123 Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile
124          215          220          225
126 TTG CTA GAT TCA CAG GGA CAC ATT GTC CTT ACT GAT TTC GGA CTC TGC      774
127 Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp Phe Gly Leu Cys

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128	230	235	240	
130	AAG GAG AAC ATT GAA CAC AAC AGC ACA ACA TCC ACC TTC TGT GGC ACG	822		
131	Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr Phe Cys Gly Thr			
132	245 250 255 260			
134	CCG GAG TAT CTC GCA CCT GAG GTG CTT CAT AAG CAG CCT TAT GAC AGG	870		
135	Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln Pro Tyr Asp Arg			
136	265 270 275			
138	ACT GTG GAC TGG TGG TGC CTG GGA GCT GTC TTG TAT GAG ATG CTG TAT	918		
139	Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu Tyr			
140	280 285 290			
142	GGC CTG CCG CCT TTT TAT AGC CGA AAC ACA GCT GAA ATG TAC GAC AAC	966		
143	Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu Met Tyr Asp Asn			
144	295 300 305			
146	ATT CTG AAC AAG CCT CTC CAG CTG AAA CCA AAT ATT ACA AAT TCC GCA	1014		
147	Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile Thr Asn Ser Ala			
148	310 315 320			
150	AGA CAC CTC CTG GAG GGC CTC CTG CAG AAG GAC AGG ACA AAG CGG CTC	1062		
151	Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg Thr Lys Arg Leu			
152	325 330 335 340			
154	GGG GCC AAG GAT GAC TTC ATG GAG ATT AAG AGT CAT GTC TTC TTC TCC	1110		
155	Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His Val Phe Phe Ser			
156	345 350 355			
158	TTA ATT AAC TGG GAT GAT CTC ATT AAT AAG AAG ATT ACT CCC CCT TTT	1158		
159	Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe			
160	360 365 370			
162	AAC CCA AAT GTG AGT GGG CCC AAC GAG CTA CGG CAC TTT GAC CCC GAG	1206		
163	Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His Phe Asp Pro Glu			
164	375 380 385			
166	TTT ACC GAA GAG CCT GTC CCC AAC TCC ATT GGC AAG TCC CCT GAC AGC	1254		
167	Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser			
168	390 395 400			
170	GTC CTC GTC ACA GCC AGC GTC AAG GAA GCT GCC GAG GCT TTC CTA GGC	1302		
171	Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu Ala Phe Leu Gly			
172	405 410 415 420			
174	TTT TCC TAT GCG CCT CCC ACG GAC TCT TTC CTC TGAACCTGT TAGGGCTTGG	1355		
175	Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu			
176	425 430			
178	TTTTAAAGGA TTTTATGTGT GTTCCGAAT GTTTTAGTTA GCCTTTTGGT GGAGCCGCCA	1415		
180	GCTGACAGGA CATCTTACAA GAGAATTTGC ACATCTCTGG AAGCTTAGCA ATCTTATTGC	1475		
182	ACACTGTTTCG CTGGAATTTT TTGAAGAGCA CATTCCTCTC AGTGAGCTCA TGAGGTTTTC	1535		
184	ATTTTTATTC TTCCTTCCAA CGTGGTGCTA TCTCTGAAAC GAGCGTTAGA GTGCCGCCCT	1595		
186	AGACGGAGGC AGGAGTTTCG TTAGAAAGCG GACCTGTTCT AAAAAAGGTC TCCTGCAGAT	1655		
188	CTGTCTGGGC TGTGATGACG AATATTATGA AATGTGCCTT TTCTGAAGAG ATTGTGTTAG	1715		
190	CTCCAAAGCT TTTCTATCG CAGTGTTCCTA GTTCTTTATT TTCCCTTGTG GATATGCTGT	1775		
192	GTGAACCGTC GTGTGAGTGT GGTATGCCTG ATCACAGATG GATTTTGTGA TAAGCATCAA	1835		
194	TGTGACACTT GCAGGACACT ACAACGTGGG ACATTGTTTG TTTCTTCCAT ATTTGAAGA	1895		
196	TAAATTATG TGTAGACTTT TTTGTAAGAT ACGGTTAATA ACTAAAATTT ATTGAAATGG	1955		
198	TCTTGCAATG ACTCGTATTC AGATGCCTAA AGAAAGCATT GCTGCTACAA ATATTCTAT	2015		
200	TTTGTAGAAAG GGTTTTATG GACCAATGCC CCAGTTGTCA GTCAGAGCCG TTGGTGTGTT	2075		

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202 TCATTGTTTA AAATGTCACC TGAAAATGG GCATTATTTA TGTTTTTTTT TTTGCATTCC 2135
204 TGATAATTGT ATGTATTGTA TAAAGAACGT CTGTACATTG GGTATAACA CTAGTATATT 2195
206 TAAACTTACA GGCTTATTTG TAATGTAAAC CACCATTTTA ATGTACTGTA ATTAACATGG 2255
208 TTATAATACG TACAATCCTT CCCTCATCCC ATCACACAAC TTTTTTTGTG TGTGATAAAC 2315
210 TGATTTTGGT TTGCAATAAA ACCTTGAAAA ATAAAAAAA AAAAAAAA AAAAA 2370
213 (2) INFORMATION FOR SEQ ID NO: 2:
215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 431 amino acids
217 (B) TYPE: amino acid
218 (D) TOPOLOGY: linear
220 (ii) MOLECULE TYPE: protein
222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
224 Met Thr Val Lys Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg
225 1 5 10 15
227 Met Arg Gly Met Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg
228 20 25 30
230 Met Gly Leu Asn Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala
231 35 40 45
233 Cys Lys His Pro Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln
234 50 55 60
236 Glu Pro Glu Leu Met Asn Ala Asn Pro Ser Pro Pro Ser Pro Ser
237 65 70 75 80
239 Gln Gln Ile Asn Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser
240 85 90 95
242 Asp Phe His Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val
243 100 105 110
245 Leu Leu Ala Arg His Lys Ala Glu Glu Val Phe Tyr Ala Val Lys Val
246 115 120 125
248 Leu Gln Lys Lys Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met
249 130 135 140
251 Ser Glu Arg Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val
252 145 150 155 160
254 Gly Leu His Phe Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu
255 165 170 175
257 Asp Tyr Ile Asn Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg
258 180 185 190
260 Cys Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser
261 195 200 205
263 Ala Leu Gly Tyr Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys
264 210 215 220
266 Pro Glu Asn Ile Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp
267 225 230 235 240
269 Phe Gly Leu Cys Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr
270 245 250 255
272 Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln
273 260 265 270
275 Pro Tyr Asp Arg Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr
276 275 280 285
278 Glu Met Leu Tyr Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu

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279      290      295      300
281 Met Tyr Asp Asn Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile
282 305      310      315      320
284 Thr Asn Ser Ala Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg
285      325      330      335
287 Thr Lys Arg Leu Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His
288      340      345      350
290 Val Phe Phe Ser Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile
291      355      360      365
293 Thr Pro Pro Phe Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His
294      370      375      380
296 Phe Asp Pro Glu Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys
297 385      390      395      400
299 Ser Pro Asp Ser Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu
300      405      410      415
302 Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
303      420      425      430
305 (2) INFORMATION FOR SEQ ID NO: 3:
307   (i) SEQUENCE CHARACTERISTICS:
308       (A) LENGTH: 19 amino acids
309       (B) TYPE: amino acid
310       (C) STRANDEDNESS:
311       (D) TOPOLOGY: linear
313   (ii) MOLECULE TYPE: peptide
318   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
320   Asp Pro Glu Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys Ser
321       1           5           10           15
323   Pro Asp Ser
326 (2) INFORMATION FOR SEQ ID NO: 4:
328   (i) SEQUENCE CHARACTERISTICS:
329       (A) LENGTH: 16 amino acids
330       (B) TYPE: amino acid
331       (C) STRANDEDNESS:
332       (D) TOPOLOGY: linear
334   (ii) MOLECULE TYPE: peptide
339   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
341   Glu Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
342       1           5           10           15

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/000,039A

DATE: 07/03/2003

TIME: 15:40:14

Input Set : N:\Crf3\RULE60\10000039A.RAW.txt

Output Set: N:\CRF4\07032003\J000039A.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)